CLAIMS

1. A method for identifying which of a plurality of different activated transcription factors are present in a biological sample, the method comprising:

contacting the biological sample with a library of transcription factor (TF) probes under conditions where TF probe – TF complexes are formed between the TF probes in the library and activated transcription factors (TFs) present in the biological sample, the TF probes each comprising a known recognition sequence varying within the library, and the TF probes in the library being capable of binding to at least two known, activated transcription factors;

isolating the TF probes that have bound to the activated TFs and formed the TF probe – TF complexes; and

contacting the isolated TF probes with an array of immobilized hybridization probes under conditions suitable for hybridization of the strands of the TF probes to the hybridization probes in the array, wherein identification of the DNA probes bound to the array identifies which of the plurality of different activated TFs are present in the biological sample.

2. The method according to claim 1, wherein each of the TF probes in the library is double-stranded DNA.

3. The method according to claim 2, wherein one strand of the double stranded TF probes further comprises a detectable marker, the method further including using the detectable marker to identify which of the isolated TF probes hybridize to the array.

4. The method according to claim 2, wherein the detectable marker is at a 5' end of the strand of the TF probes.

5. The method according to claim 2, wherein the detectable marker is biotin at a 5' end of the strand of the TF probes.

6. The method according to claim 1, wherein the library comprises TF probes having recognition sequences between 10 and 100 base pairs in length.

7. The method according to claim 1, wherein the library comprises TF probes having recognition sequences between 20 and 40 base pairs in length.

8. The method according to claim 1, wherein the library comprises TF probes having recognition sequences between 25 and 35 base pairs in length.

9. The method according to claim 1, wherein the library comprises TF probes having at least 2 different recognition sequences.

10. The method according to claim 1, wherein the library comprises TF probes having at least 5 different recognition sequences.

11. The method according to claim 1, wherein the library comprises TF probes having at least 10 different recognition sequences.

12. The method according to claim 1, wherein the library comprises TF probes having at least 20 different recognition sequences.

13. The method according to claim 1, wherein the library comprises TF probes having at least 50 different recognition sequences.

14. The method according to claim 1, wherein the recognition sequences in the library of TF probes are for recognizing activated transcription factors from at least 2 different types of cells.

15. The method according to claim 1, wherein the recognition sequences in the library of TF probes are for recognizing activated transcription factors from at least 5 different types of cells.

16. The method according to claim 1, wherein the recognition sequences in the library of TF probes are for recognizing activated transcription factors from at least 10 different types of cells.

17. The method according to claim 1, wherein the recognition sequences in the library of TF probes are for recognizing activated transcription factors from malignant, benign, and normal cell types.

18. The method according to claim 1, wherein the biological sample is a nuclear extract of cells.

19. The method according to claim 1, wherein each of the immobilized hybridization probes comprises at least two copies of a complement to a portion of the recognition sequence comprised on TF probe.

20. The method according to claim 1, wherein the recognition sequences comprised on the TF probes are known to bind to at least two TFs selected from the group consisting of NF-E1, NFκB, Ets, Ap1, p53 and c-Myb.

21. The method according to claim 1, wherein the recognition sequences comprised on the TF probes are known to bind to at least two TFs selected from the group consisting of AP1, AP-2, ARE, Brn-3, C/EBP, CBF, CDP, c-Myb, CREB, E2F-1, EFR, ERE, Ets-1/PEA3, FAST-1, GAS/ISRE, GATA, GRE, HNF-4, IRF-1, MEF-1, MEF-2, Myc-Max, NF-1, NFATc, NF-E2, NFκB, Oct-1, p53, Pax-5, Pbx1, Pit 1, PPAR, PRE, RAR, RAR (DR-5), SIE, Smad SBE, Smad3/4, SP1, SRE, Stat1, Stat3, Stat4, Stat4, Stat5, Stat6, TFIID, TR, TR(DR-4), USF-1, VDR (DR-3), HSE, and MRE;

22. A method for identifying multiple different transcription factors present in a biological sample, the method comprising:

mixing the biological sample with a library of transcription factor (TF) probes under suitable conditions such that the TF probes bind to the transcription factors (TFs) in the biological sample, each of the TF probes comprising a known recognition sequence varying within the library, and the TF probes in the library being capable of binding to at least two known TFs;

isolating the TF probes that have bound to the transcription factors; and

determining identities of isolated TF probes, determination of the identities identifying which TFs are present in the biological sample.

23. The method according to claim 22, wherein the TF probes are double-stranded DNA.

24. The method according to claim 22, wherein the step of determining includes:

sequencing the isolated TF probes, sequences of the TF probes identifying which TFs are present in the biological sample.

25. The method according to claim 22, wherein the step of determining includes:

identifying the isolated TF probes by mass spectroscopy.

26. The method according to claim 22, wherein the step of determining includes:

identifying the isolated TF probes by electrophoresis.

27. The method according to claim 22, wherein the library comprises TF probes having recognition sequences between 20 and 40 base pairs in length.

28. The method according to claim 22, wherein the library comprises TF probes having at least 2 different recognition sequences.

29. The method according to claim 22, wherein the library comprises TF probes having at least 5 different recognition sequences.

30. The method according to claim 22, wherein the library comprises TF probes having at least 10 different recognition sequences.

31. The method according to claim 22, wherein the recognition sequences in the library of TF probes are for recognizing transcription factors from at least 2 different types of cells.

32. The method according to claim 22, wherein the recognition sequences in the library of TF probes are for recognizing transcription factors from at least 5 different types of cells.

33. The method according to claim 22, wherein the recognition sequences in the library of TF probes are for recognizing transcription factors from at least 10 different types of cells.

34. The method according to claim 22, wherein the recognition sequences in the library of TF probes are for recognizing TFs from malignant, benign, and normal cell types.

35. The method according to claim 22, wherein the recognition sequences comprised on the TF probes are known to bind to at least two TFs selected from the group consisting of AP1, AP-2, ARE, Brn-3, C/EBP, CBF, CDP, c-Myb, CREB, E2F-1, EFR, ERE, Ets, Ets-1/PEA3, FAST-1, GAS/ISRE, GATA, GRE, HNF-4, IRF-1, MEF-1, MEF-2, Myc-Max, NF-1, NFATc, NF-E1, NF-E2, NFκB, Oct-1, p53, Pax-5, Pbx1, Pit 1, PPAR, PRE, RAR, RAR (DR-5), SIE, Smad SBE, Smad3/4, SP1, SRE, Stat1, Stat3, Stat4, Stat4, Stat5, Stat6, TFIID, TR, TR(DR-4), USF-1, VDR (DR-3), HSE, and MRE.

36. The method according to claim 22, wherein the biological sample is a nuclear extract of cells.